IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: SALK1720-6

In re patent application of

MATHEWS, LAWRENCE S. *et al.*

Serial No. 09/742,684

Filed: December 19, 2000

For: CLONING AND RECOMBINANT PRODUCTION OF RECEPTOR(S) OF
    THE ACTIVIN/TGF-BETA SUPERFAMILY

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C.   20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1.   the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;
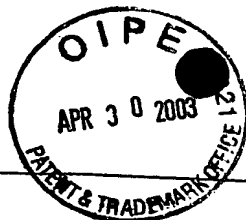
2.   the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same.

Respectfully submitted,

April 22, 2003

Date

David M. Narkunas
Reg. No. 53,370

HARBOR CONSULTING IP SERVICES, INC.
1500A Lafayette Road, #262
Portsmouth, N.H.
800-318-3021

SEQUENCE LISTING

<110> MATHEWS, LAWRENCE S.
      VALE JR., WYLIE W.
      TSUCHIDA, KUNIHIRO

<120> CLONING AND RECOMBINANT PRODUCTION OF RECEPTOR(S) OF
      THE ACTIVIN/TGF-BETA SUPERFAMILY

<130> SALK1720-6

<140> 09/742,684
<141> 2000-12-19

<150> 08/476,123
<151> 1995-06-07

<150> 08/300,584
<151> 1994-09-02

<150> 07/880,220
<151> 1992-05-08

<150> 07/773,229
<151> 1991-10-09

<150> 07/698,709
<151> 1991-05-10

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 2563
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (71)..(1609)

<400> 1
ctccgaggaa gacccaggga actggatatc tagcgagaac ttcctacggc ttctccggcg   60

cctcgggaaa atg gga gct gct gca aag ttg gcg ttc gcc gtc ttt ctt   109
            Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu
             1   5   10

atc tct tgc tct tca ggt gct ata ctt ggc aga tca gaa act cag gag   157
Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu
    15   20   25

tgt ctt ttc ttt aat gct aat tgg gaa aga gac aga acc aac cag act   205
Cys Leu Phe Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr
30   35   40   45

```
ggt gtt gaa cct tgc tat ggt gat aaa gat aaa cgg cga cat tgt ttt    253
Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe
                50                  55                  60

gct acc tgg aag aat att tct ggt tcc att gaa ata gtg aag caa ggt    301
Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly
                65                  70                  75

tgt tgg ctg gat gat atc aac tgc tat gac agg act gat tgt ata gaa    349
Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu
            80                  85                  90

aaa aaa gac agc cct gaa gtg tac ttt tgt tgc tgt gag ggc aat atg    397
Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met
        95                  100                 105

tgt aat gaa aag ttc tct tat ttt ccg gag atg gaa gtc aca cag ccc    445
Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro
110             115                 120                 125

act tca aat cct gtt aca ccg aag cca ccc tat tac aac att ctg ctg    493
Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu
                130                 135                 140

tat tcc ttg gta cca cta atg tta att gca gga att gtc att tgt gca    541
Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala
                145                 150                 155

ttt tgg gtg tac aga cat cac aag atg gcc tac cct cct gta ctt gtt    589
Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val
                160                 165                 170

cct act caa gac cca gga cca ccc cca cct tcc cca tta cta ggg ttg    637
Pro Thr Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu
                175                 180                 185

aag cca ttg cag ctg tta gaa gtg aaa gca agg gga aga ttt ggt tgt    685
Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys
190                 195                 200                 205

gtc tgg aaa gcc cag ttg ctc aat gaa tat gtg gct gtc aaa ata ttt    733
Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe
                210                 215                 220

cca ata cag gac aaa cag tcc tgg cag aat gaa tat gaa gtc tat agt    781
Pro Ile Gln Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser
                225                 230                 235

cta cct gga atg aag cat gag aac ata cta cag ttc att ggt gca gag    829
Leu Pro Gly Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu
                240                 245                 250

aaa aga ggc acc agt gtg gat gtg gac ctg tgg cta atc aca gca ttt    877
Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe
                255                 260                 265
```

```
cat gaa aag ggc tca ctg tca gac ttt ctt aag gct aat gtg gtc tct   925
His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser
270             275             280                 285

tgg aat gaa ctt tgt cat att gca gaa acc atg gct aga gga ttg gca   973
Trp Asn Glu Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala
                290             295             300

tat tta cat gag gat ata cct ggc tta aaa gat ggc cac aag cct gca   1021
Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala
            305             310             315

atc tct cac agg gac atc aaa agt aaa aat gtg ctg ttg aaa aac aat   1069
Ile Ser His Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn
        320             325             330

ctg aca gct tgc att gct gac ttt ggg ttg gcc tta aag ttc gag gct   1117
Leu Thr Ala Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala
    335             340             345

ggc aag tct gca ggt gac acc cat ggg cag gtt ggt acc cgg agg tat   1165
Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr
350             355             360             365

atg gct cca gag gtg ttg gag ggt gct ata aac ttc caa agg gac gca   1213
Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala
                370             375             380

ttt ctg agg ata gat atg tac gcc atg gga tta gtc cta tgg gaa ttg   1261
Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu
            385             390             395

gct tct cgt tgc act gct gca gat gga ccc gta gat gag tac atg tta   1309
Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu
        400             405             410

cca ttt gag gaa gaa att ggc cag cat cca tct ctt gaa gat atg cag   1357
Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln
    415             420             425

gaa gtt gtt gtg cat aaa aaa aag agg cct gtt tta aga gat tat tgg   1405
Glu Val Val Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp
430             435             440             445

cag aaa cat gca gga atg gca atg ctc tgt gaa acg ata gaa gaa tgt   1453
Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys
                450             455             460

tgg gat cat gat gca gaa gcc agg tta tca gct gga tgt gta ggt gaa   1501
Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu
            465             470             475

aga att act cag atg caa aga cta aca aat atc att act aca gag gac   1549
Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp
        480             485             490
```

```
att gta aca gtg gtc aca atg gtg aca aat gtt gac ttt cct ccc aaa   1597
Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
    495             500             505

gaa tct agt cta tgatggtggc accgtctgta cacactgagg actgggactc      1649
Glu Ser Ser Leu
510

tgaactggag ctgctaagct aaggaaagtg cttagttgat tttctgtgtg aaatgagtag 1709

gatgcctcca ggacatgtac gcaagcagcc ccttgtggaa agcatggatc tgggagatgg 1769

atctgggaaa cttactgcat cgtctgcagc acagatatga agaggagtct aagggaaaag 1829

ctgcaaactg taaagaactt ctgaaaatgt actcgaagaa tgtggccctc tccaaatcaa 1889

ggatcttttg gacctggcta atcaagtatt tgcaaaactg acatcagatt tcttaatgtc 1949

tgtcagaaga cactaattcc ttaaatgaac tactgctatt tttttaaat gaaaaacttt 2009

tcatttcaga ttttaaaaag ggtaactttt tattgcattt gctgttgttt ctataaatga 2069

ctattgtaat gccaacatga cacagcttgt gaatgtgtag tgtgctgctg ttctgtgtac 2129

atagtcatca aagtggggta cagtaaagag gcttccaagc attactttaa cctccctcaa 2189

caaggtatac ctcagttcca cggttgttaa attataaaat tgaaaacact aacagaattt 2249

gaataaatca gtccatgttt tataacaagg ttaattacaa attcactgtg ttatttaaga 2309

aaaaatggta agctatgctt agtgccaata gtaagtggct atttgtaaag cagtgtttta 2369

gcttttcttc tactggcttg taatttaggg aaaacaagtg ctgtctttga aatggaaaag 2429

aatatggtgt caccctaccc cccatactta tatcaaggtc ccaaaatatt cttttccatt 2489

tcaaagacag cactttgaaa accctaaatt acaagccagt agaagaaaag ctaaaacacg 2549

ctttacaaat agcc                                                  2563
```

```
<210> 2
<211> 513
<212> PRT
<213> Mus sp.

<400> 2
Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
1               5                   10                  15

Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
            20                  25                  30

Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr Gly Val Glu
        35                  40                  45

Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
    50                  55                  60
```

```
Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
65              70          75              80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu Lys Lys Asp
              85          90              95

Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
          100         105             110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
        115         120             125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
    130         135             140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
145             150             155             160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
            165             170             175

Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
        180             185             190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
        195             200             205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
        210             215             220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
225             230             235             240

Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
            245             250             255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
            260             265             270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
        275             280             285

Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
    290             295             300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
305             310             315             320

Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
            325             330             335

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
            340             345             350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
        355             360             365
```

```
Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
    370             375             380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
385             390             395             400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
            405             410             415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
            420             425             430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
        435             440             445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
    450             455             460

Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
465             470             475             480

Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
            485             490             495

Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
        500             505             510

Leu


<210> 3
<211> 2335
<212> DNA
<213> Xenopus sp.

<220>
<221> CDS
<222> (468)..(1997)

<400> 3
ccgcccacac agtgcagtga ataatagccg gtgcggcccc tcccctcttt ccctggcagt 60

tgtgtatctg tcacattgaa gtttgggctc ctgtgagtct gagcctcccc ctgtgtctca 120

tgtgaagctg ctgctgcaga aggtggagtc gttgcatgag ggtgggggga gtcgctgctg 180

tttgatctgc ctctgctccc cattcacact ctcatttcat tcccacggat ccacattaca 240

actcgccttt aacccttttcc ctggcggagc ccacgcgtct ttcatccctc ctgccgcggc 300

cgctgagcga ccagagcgcg acattgttgc ggcggggggat tgggcgacat tgttgcgaat 360

aatcggagct gctggggggg aactgataca acgttgcgac tgtaaaggaa ttaactcggc 420

cgaatgggat tttatctgtg tcggtgagag aagcggatcc caggagc atg ggg gcg   476
                                                      Met Gly Ala
                                                       1
```

```
tct gta gcg ctg act ttt cta ctt ctt ctt gca act ttc cgc gca ggc    524
Ser Val Ala Leu Thr Phe Leu Leu Leu Leu Ala Thr Phe Arg Ala Gly
     5                  10                  15

tca gga cac gat gaa gtg gag aca aga gag tgc atc tat tac aat gcc    572
Ser Gly His Asp Glu Val Glu Thr Arg Glu Cys Ile Tyr Tyr Asn Ala
 20                  25                  30                  35

aac tgg gaa ctg gag aag acc aac caa agt ggg gtg gaa agc tgc gaa    620
Asn Trp Glu Leu Glu Lys Thr Asn Gln Ser Gly Val Glu Ser Cys Glu
                 40                  45                  50

ggg gaa aag gac aag cga ctc cac tgt tac gcg tct tgg agg aac aat    668
Gly Glu Lys Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg Asn Asn
             55                  60                  65

tcg ggc ttc ata gag ctg gtg aaa aaa gga tgc tgg ctg gat gac ttc    716
Ser Gly Phe Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp Asp Phe
         70                  75                  80

aac tgt tat gac aga cag gaa tgt att gcc aag gaa gaa aac ccc caa    764
Asn Cys Tyr Asp Arg Gln Glu Cys Ile Ala Lys Glu Glu Asn Pro Gln
     85                  90                  95

gtc ttt ttc tgc tgc tgc gag gga aac tac tgc aac aag aaa ttt act    812
Val Phe Phe Cys Cys Cys Glu Gly Asn Tyr Cys Asn Lys Lys Phe Thr
100                 105                 110                 115

cat ttg cct gaa gtc gaa aca ttt gat ccg aag ccc cag ccg tca gcc    860
His Leu Pro Glu Val Glu Thr Phe Asp Pro Lys Pro Gln Pro Ser Ala
                120                 125                 130

tcc gta ctg aac att ctg atc tat tcc ctg ctt cca att gtt ggt ctt    908
Ser Val Leu Asn Ile Leu Ile Tyr Ser Leu Leu Pro Ile Val Gly Leu
             135                 140                 145

tcc atg gca att ctc ctg gcg ttc tgg atg tac cgt cat cga aag cct    956
Ser Met Ala Ile Leu Leu Ala Phe Trp Met Tyr Arg His Arg Lys Pro
         150                 155                 160

ccc tac ggg cat gta gag atc aat gag gac ccc ggt ctg ccc cct cca    1004
Pro Tyr Gly His Val Glu Ile Asn Glu Asp Pro Gly Leu Pro Pro Pro
         165                 170                 175

tct cct ctg gtc ggg ctg aag ccg ctg cag ttg ctg gag ata aag gcg    1052
Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala
180                 185                 190                 195

cga ggc cgt ttc ggt tgc gtc tgg aaa gct cgt ctg ctg aat gaa tat    1100
Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Arg Leu Leu Asn Glu Tyr
                 200                 205                 210

gtc gca gtg aaa atc ttc ccc gtg cag gat aag cag tcg tgg cag tgt    1148
Val Ala Val Lys Ile Phe Pro Val Gln Asp Lys Gln Ser Trp Gln Cys
             215                 220                 225
```

```
gag aaa gag atc ttc acc acg ccg ggc atg aaa cat gaa aac cta ttg      1196
Glu Lys Glu Ile Phe Thr Thr Pro Gly Met Lys His Glu Asn Leu Leu
        230             235             240

gag ttc att gcc gct gag aag agg gga agc aac ctg gag atg gag ctg      1244
Glu Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Met Glu Leu
        245             250             255

tgg ctc atc act gca ttt cat gat aag ggt tct ctg acg gac tac ctg      1292
Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu
260             265             270             275

aaa ggg aac ttg gtg agc tgg aat gaa ctg tgt cac ata aca gaa aca      1340
Lys Gly Asn Leu Val Ser Trp Asn Glu Leu Cys His Ile Thr Glu Thr
        280             285             290

atg gct cgt ggg ctg gcc tac tta cat gaa gat gtg ccc cgc tgt aaa      1388
Met Ala Arg Gly Leu Ala Tyr Leu His Glu Asp Val Pro Arg Cys Lys
        295             300             305

ggt gaa ggg cac aaa cct gca atc gct cac aga gat ttt aaa agt aag      1436
Gly Glu Gly His Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Lys
        310             315             320

aat gta ttg cta aga aac gac ctg act gcg ata tta gca gac ttc ggg      1484
Asn Val Leu Leu Arg Asn Asp Leu Thr Ala Ile Leu Ala Asp Phe Gly
        325             330             335

ctg gcc gta cga ttt gag cct gga aaa cct ccg gga gat aca cac ggg      1532
Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly
340             345             350             355

cag gtt ggc acc agg agg tat atg gct cct gag gtt cta gag gga gca      1580
Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala
        360             365             370

att aac ttt cag cga gat tcc ttt ctc agg ata gat atg tat gcc atg      1628
Ile Asn Phe Gln Arg Asp Ser Phe Leu Arg Ile Asp Met Tyr Ala Met
        375             380             385

gga ctg gta ctc tgg gaa ata gta tcc cga tgt aca gca gca gat ggg      1676
Gly Leu Val Leu Trp Glu Ile Val Ser Arg Cys Thr Ala Ala Asp Gly
        390             395             400

cca gta gat gag tat ctg ctc cca ttc gaa gaa gag att ggg caa cat      1724
Pro Val Asp Glu Tyr Leu Leu Pro Phe Glu Glu Glu Ile Gly Gln His
        405             410             415

cct tcc cta gag gat ctg caa gaa gtt gtc gtt cac aag aag ata cgc      1772
Pro Ser Leu Glu Asp Leu Gln Glu Val Val Val His Lys Lys Ile Arg
420             425             430             435

cct gta ttc aaa gac cac tgg ctg aaa cac cct ggt ctg gcc caa ctg      1820
Pro Val Phe Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu
        440             445             450
```

```
tgc gtc acc att gaa gaa tgc tgg gac cat gat gcg gaa gca cgg ctt    1868
Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu
            455                 460                 465

tcg gca ggc tgc gta gag gag cgt att tcc caa atc cgt aaa tca gtg    1916
Ser Ala Gly Cys Val Glu Glu Arg Ile Ser Gln Ile Arg Lys Ser Val
            470                 475                 480

aac ggc act acc tcg gac tgc ctt gta tcc att gtt aca tct gtc acc    1964
Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Ile Val Thr Ser Val Thr
            485                 490                 495

aat gtg gac ttg ccg ccc aaa gag tcc agt atc tgaggtttct ttggtctttc  2017
Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
500                 505                 510

cagactcagt gactttaaa aaaaaaactc acgaatgcag ctgctatttt atcttgactt    2077

tttaatattt tttttcttgg attttacttg gatcggatca atttaccagc acgtcattcg    2137

aaagtattaa aaaaaaaaaa caaaacaaaa aagcaaaaac agacatctca gcaagcattc    2197

aggtgccgac ttatgaatgc caataggtgc aggaacttca gaacctcaac aaactcattt    2257

ctagagaatg ttctcctggt ttcctttatc tcagaagagg acccatagga aaacacctaa    2317

gtcaagcaaa tgctgcag                                                 2335
```

```
<210> 4
<211> 510
<212> PRT
<213> Xenopus sp.

<400> 4
Met Gly Ala Ser Val Ala Leu Thr Phe Leu Leu Leu Ala Thr Phe
  1           5               10                15

Arg Ala Gly Ser Gly His Asp Glu Val Glu Thr Arg Glu Cys Ile Tyr
            20                  25                  30

Tyr Asn Ala Asn Trp Glu Leu Glu Lys Thr Asn Gln Ser Gly Val Glu
            35                  40                  45

Ser Cys Glu Gly Glu Lys Asp Lys Arg Leu His Cys Tyr Ala Ser Trp
      50                  55                  60

Arg Asn Asn Ser Gly Phe Ile Glu Leu Val Lys Lys Gly Cys Trp Leu
65                  70                  75                  80

Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Ile Ala Lys Glu Glu
                  85                  90                  95

Asn Pro Gln Val Phe Phe Cys Cys Cys Glu Gly Asn Tyr Cys Asn Lys
                  100                 105                 110

Lys Phe Thr His Leu Pro Glu Val Glu Thr Phe Asp Pro Lys Pro Gln
            115                 120                 125
```

Pro Ser Ala Ser Val Leu Asn Ile Leu Ile Tyr Ser Leu Leu Pro Ile
130   135   140

Val Gly Leu Ser Met Ala Ile Leu Leu Ala Phe Trp Met Tyr Arg His
145   150   155   160

Arg Lys Pro Pro Tyr Gly His Val Glu Ile Asn Glu Asp Pro Gly Leu
165   170   175

Pro Pro Pro Ser Pro Leu Val Gly Leu Lys Pro Leu Gln Leu Leu Glu
180   185   190

Ile Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala Arg Leu Leu
195   200   205

Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Val Gln Asp Lys Gln Ser
210   215   220

Trp Gln Cys Glu Lys Glu Ile Phe Thr Thr Pro Gly Met Lys His Glu
225   230   235   240

Asn Leu Leu Glu Phe Ile Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu
245   250   255

Met Glu Leu Trp Leu Ile Thr Ala Phe His Asp Lys Gly Ser Leu Thr
260   265   270

Asp Tyr Leu Lys Gly Asn Leu Val Ser Trp Asn Glu Leu Cys His Ile
275   280   285

Thr Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu Asp Val Pro
290   295   300

Arg Cys Lys Gly Glu Gly His Lys Pro Ala Ile Ala His Arg Asp Phe
305   310   315   320

Lys Ser Lys Asn Val Leu Leu Arg Asn Asp Leu Thr Ala Ile Leu Ala
325   330   335

Asp Phe Gly Leu Ala Val Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp
340   345   350

Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro Glu Val Leu
355   360   365

Glu Gly Ala Ile Asn Phe Gln Arg Asp Ser Phe Leu Arg Ile Asp Met
370   375   380

Tyr Ala Met Gly Leu Val Leu Trp Glu Ile Val Ser Arg Cys Thr Ala
385   390   395   400

Ala Asp Gly Pro Val Asp Glu Tyr Leu Leu Pro Phe Glu Glu Glu Ile
405   410   415

Gly Gln His Pro Ser Leu Glu Asp Leu Gln Glu Val Val Val His Lys
420   425   430

```
Lys Ile Arg Pro Val Phe Lys Asp His Trp Leu Lys His Pro Gly Leu
        435             440                 445

Ala Gln Leu Cys Val Thr Ile Glu Glu Cys Trp Asp His Asp Ala Glu
        450             455                 460

Ala Arg Leu Ser Ala Gly Cys Val Glu Glu Arg Ile Ser Gln Ile Arg
465                 470                 475                 480

Lys Ser Val Asn Gly Thr Thr Ser Asp Cys Leu Val Ser Ile Val Thr
                485                 490                 495

Ser Val Thr Asn Val Asp Leu Pro Pro Lys Glu Ser Ser Ile
                500             505                 510
```

<210> 5
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<400> 5
Asp Leu Lys Pro Glu Asn
  1   5

<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<220>
<221> MOD_RES
<222> (2)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (3)..(4)
<223> Variable amino acid

<220>
<221> MOD_RES
<222> (5)
<223> Tyr or Phe

<220>
<221> MOD_RES

```
<222> (6)
<223> Variable amino acid

<400> 6
Gly Xaa Xaa Xaa Xaa Xaa
  1               5


<210> 7
<211> 6
<212> PRT
<213> Homo sapiens

<400> 7
Asp Ile Lys Ser Lys Asn
  1               5


<210> 8
<211> 6
<212> PRT
<213> Homo sapiens

<400> 8
Gly Thr Arg Arg Tyr Met
  1               5


<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<400> 9
Asp Leu Ala Ala Arg Asn
  1               5


<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<220>
<221> MOD_RES
<222> (1)
<223> Variable amino acid

<220>
<221> MOD_RES
```

```
<222> (3)
<223> Ile or Val

<220>
<221> MOD_RES
<222> (4)
<223> Lys or Arg

<220>
<221> MOD_RES
<222> (6)
<223> Thr or Met

<400> 10
Xaa Pro Xaa Xaa Trp Xaa
  1                   5


<210> 11
<211> 1602
<212> DNA
<213> Rattus sp.

<220>
<221> CDS
<222> (72)..(1550)

<400> 11
ccccgggaac ttcaaagcgc gctgcggcgg cgctctggga ccccgaagcc ttgcaccgcc  60

gcggggtggc c atg acc cca gcg cgc cgc tcc gca ctg agc ctg gcc ctc  110
             Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu
               1               5                  10

ctg ctg gtg gca ctg gcc tcc gac ctt gcg gca gga ctg aag tgt gtg  158
Leu Leu Val Ala Leu Ala Ser Asp Leu Ala Ala Gly Leu Lys Cys Val
     15                  20                  25

tgt ctt ttg tgt gat tcc tca aac ttt acc tgc caa acc gaa gga gca  206
Cys Leu Leu Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala
 30                  35                  40                  45

tgc tgg gcc tct gtc atg cta acc aac ggg aaa gaa cag gtg agc aaa  254
Cys Trp Ala Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ser Lys
             50                  55                  60

tcg tgc gtg tcc ctc ccg gaa cta aat gct cag gtc ttc tgt cac agt  302
Ser Cys Val Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser
             65                  70                  75

tcc aac aac gtg acc aag acc gaa tgt tgc ttc aca gac ttc tgc aac  350
Ser Asn Asn Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn
             80                  85                  90

aac atc act cag cac ctt ccc aca gca tct cca gat gcc cct aga ctt  398
Asn Ile Thr Gln His Leu Pro Thr Ala Ser Pro Asp Ala Pro Arg Leu
     95                  100                 105
```

14

ggc ccc aca gag ctg aca gtt gtt atc act gta cct gtt tgc ctc ctg   446
Gly Pro Thr Glu Leu Thr Val Val Ile Thr Val Pro Val Cys Leu Leu
110   115   120   125

tcc atc gca gcc atg cta acg ata tgg gcc tgc cag gac cgc cag tgc   494
Ser Ile Ala Ala Met Leu Thr Ile Trp Ala Cys Gln Asp Arg Gln Cys
                130   135   140

aca tac agg aag acc aag aga cac aat gtg gag gaa cca ctg gca gag   542
Thr Tyr Arg Lys Thr Lys Arg His Asn Val Glu Glu Pro Leu Ala Glu
                145   150   155

tac agc ctt gtc aat gct gga aaa acc ctc aaa gat ctg att tat gat   590
Tyr Ser Leu Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp
                160   165   170

gcc act gcc tcg ggc tca gga tct ggc ccg cct ctt ttg gtt caa aga   638
Ala Thr Ala Ser Gly Ser Gly Ser Gly Pro Pro Leu Leu Val Gln Arg
        175   180   185

acc atc gca agg aca att gta ctt caa gaa atc gta gga aaa ggt cgg   686
Thr Ile Ala Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg
190   195   200   205

ttt ggg gaa gtg tgg cac gga aga tgg tgt gga gaa gat gtg gct gtg   734
Phe Gly Glu Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val
                210   215   220

aaa ata ttc tcc tcc aga gat gag aga tct tgg ttc cgt gag gca gaa   782
Lys Ile Phe Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu
                225   230   235

att tat cag acg gta atg ctg aga cat gag aat att ctc ggt ttc atc   830
Ile Tyr Gln Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile
                240   245   250

gcg gcc gac aac aaa gat aat gga acc tgg act cag ctt tgg ctt gtg   878
Ala Ala Asp Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val
        255   260   265

tca gag tat cac gag cag ggc tcc tta tat gac tat ttg aat aga aac   926
Ser Glu Tyr His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn
270   275   280   285

ata gtg acc gtg gct gga atg gtc aag ttg gcg ctt tca ata gcg agt   974
Ile Val Thr Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser
        290   295   300

ggt ctg gct cac cta cac atg gag atc gtg ggc act caa ggt aag cct   1022
Gly Leu Ala His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro
        305   310   315

gct att gct cac cga gat ata aag tca aag aat atc tta gtc aaa aag   1070
Ala Ile Ala His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys
        320   325   330

```
tgt gac act tgt gcc ata gct gac tta ggg ctg gct gtg aaa cat gat      1118
Cys Asp Thr Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp
    335                 340                 345

tct atc atg aac act ata gat ata ccc cag aat cct aaa gtg gga acc      1166
Ser Ile Met Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr
350                 355                 360                 365

aag agg tat atg gct ccc gaa atg ctt gat gat aca atg aac gtc aac      1214
Lys Arg Tyr Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn
                370                 375                 380

atc ttt gag tcc ttc aag cga gct gac atc tat tcg gtg ggg ctg gtt      1262
Ile Phe Glu Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val
            385                 390                 395

tac tgg gaa ata gct cga agg tgt tca gtt gga gga ctt gtt gaa gag      1310
Tyr Trp Glu Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu
        400                 405                 410

tac cag ttg cct tat tat gac atg gtg cct tca gat cct tcc ata gag      1358
Tyr Gln Leu Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu
    415                 420                 425

gaa atg agg aag gtc gtt tgt gat cag aaa ctg cga cca aat ctc cca      1406
Glu Met Arg Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro
430                 435                 440                 445

aac cag tgg caa agc tgt gag gcg ctc cgg gtc atg gga aga ata atg      1454
Asn Gln Trp Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met
                450                 455                 460

cgt gag tgc tgg tat gcc aac ggg gca gct cgc ctg acc gcc ctg cgc      1502
Arg Glu Cys Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg
            465                 470                 475

gtg aag aag acc att tct cag ctg tgt gtc aag gaa gac tgt aag gcc      1550
Val Lys Lys Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
        480                 485                 490

taaggataca ggcgacggga aagccctcac cactctcttt catgtctcct gc            1602
```

```
<210> 12
<211> 493
<212> PRT
<213> Rattus sp.

<400> 12
Met Thr Pro Ala Arg Arg Ser Ala Leu Ser Leu Ala Leu Leu Leu Val
  1               5                  10                  15

Ala Leu Ala Ser Asp Leu Ala Ala Gly Leu Lys Cys Val Cys Leu Leu
               20                  25                  30

Cys Asp Ser Ser Asn Phe Thr Cys Gln Thr Glu Gly Ala Cys Trp Ala
           35                  40                  45
```

Ser Val Met Leu Thr Asn Gly Lys Glu Gln Val Ser Lys Ser Cys Val
    50   55   60

Ser Leu Pro Glu Leu Asn Ala Gln Val Phe Cys His Ser Ser Asn Asn
65   70   75   80

Val Thr Lys Thr Glu Cys Cys Phe Thr Asp Phe Cys Asn Asn Ile Thr
             85   90   95

Gln His Leu Pro Thr Ala Ser Pro Asp Ala Pro Arg Leu Gly Pro Thr
        100   105   110

Glu Leu Thr Val Val Ile Thr Val Pro Val Cys Leu Leu Ser Ile Ala
       115   120   125

Ala Met Leu Thr Ile Trp Ala Cys Gln Asp Arg Gln Cys Thr Tyr Arg
       130   135   140

Lys Thr Lys Arg His Asn Val Glu Glu Pro Leu Ala Glu Tyr Ser Leu
145   150   155   160

Val Asn Ala Gly Lys Thr Leu Lys Asp Leu Ile Tyr Asp Ala Thr Ala
          165   170   175

Ser Gly Ser Gly Ser Gly Pro Pro Leu Leu Val Gln Arg Thr Ile Ala
        180   185   190

Arg Thr Ile Val Leu Gln Glu Ile Val Gly Lys Gly Arg Phe Gly Glu
       195   200   205

Val Trp His Gly Arg Trp Cys Gly Glu Asp Val Ala Val Lys Ile Phe
       210   215   220

Ser Ser Arg Asp Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln
225   230   235   240

Thr Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp
          245   250   255

Asn Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Glu Tyr
        260   265   270

His Glu Gln Gly Ser Leu Tyr Asp Tyr Leu Asn Arg Asn Ile Val Thr
        275   280   285

Val Ala Gly Met Val Lys Leu Ala Leu Ser Ile Ala Ser Gly Leu Ala
       290   295   300

His Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala
305   310   315   320

His Arg Asp Ile Lys Ser Lys Asn Ile Leu Val Lys Lys Cys Asp Thr
       325   330   335

Cys Ala Ile Ala Asp Leu Gly Leu Ala Val Lys His Asp Ser Ile Met
       340   345   350

```
Asn Thr Ile Asp Ile Pro Gln Asn Pro Lys Val Gly Thr Lys Arg Tyr
        355             360             365

Met Ala Pro Glu Met Leu Asp Asp Thr Met Asn Val Asn Ile Phe Glu
    370             375             380

Ser Phe Lys Arg Ala Asp Ile Tyr Ser Val Gly Leu Val Tyr Trp Glu
385             390             395             400

Ile Ala Arg Arg Cys Ser Val Gly Gly Leu Val Glu Glu Tyr Gln Leu
            405             410             415

Pro Tyr Tyr Asp Met Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg
            420             425             430

Lys Val Val Cys Asp Gln Lys Leu Arg Pro Asn Leu Pro Asn Gln Trp
        435             440             445

Gln Ser Cys Glu Ala Leu Arg Val Met Gly Arg Ile Met Arg Glu Cys
    450             455             460

Trp Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Val Lys Lys
465             470             475             480

Thr Ile Ser Gln Leu Cys Val Lys Glu Asp Cys Lys Ala
            485             490
```

```
<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (11)
<223> a, t, c or g

<220>
<221> modified_base
<222> (14)
<223> a, t, c or g

<220>
<221> modified_base
<222> (17)
<223> a, t, c or g

<400> 13
cgggatccgt ngcngtnaar athttycc                                    28


<210> 14
<211> 35
```

```
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (12)
<223> a, t, c or g

<220>
<221> modified_base
<222> (15)
<223> a, t, c or g

<220>
<221> modified_base
<222> (24)
<223> a, t, c or g

<220>
<221> modified_base
<222> (30)
<223> a, t, c or g

<220>
<221> modified_base
<222> (33)
<223> a, t, c or g

<400> 14
cgggatccyt cnggngccat rtanckyctn gtncc                              35


<210> 15
<211> 2563
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (71)..(1609)

<220>
<221> modified_base
<222> (346)
<223> a, t, c or g

<400> 15
ctccgaggaa gacccaggga actggatatc tagcgagaac ttcctacggc ttctccggcg 60

cctcgggaaa atg gga gct gct gca aag ttg gcg ttc gcc gtc ttt ctt    109
             Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu
              1               5                   10
```

```
atc tct tgc tct tca ggt gct ata ctt ggc aga tca gaa act cag gag   157
Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu
        15                  20                  25

tgt ctt ttc ttt aat gct aat tgg gaa aar gac aga acc aac cag act   205
Cys Leu Phe Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr
 30                  35                  40                      45

ggt gtt gaa cct tgc tat ggt gat aaa gat aaa cgg cga cat tgt ttt   253
Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe
                50                  55                  60

gct acc tgg aag aat att tct ggt tcc att gaa ata gtg aag caa ggt   301
Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly
            65                  70                  75

tgt tgg ctg gat gat atc aac tgc tat gac agg act gat tgt gtn gaa   349
Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu
        80                  85                  90

aaa aaa gac agc cct gaa gtg tac ttt tgt tgc tgt gag ggc aat atg   397
Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met
    95                  100                 105

tgt aat gaa aag ttc tct tat ttt ccg gag atg gaa gtc aca cag ccc   445
Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro
110                 115                 120                 125

act tca aat cct gtt aca ccg aag cca ccc tat tac aac att ctg ctg   493
Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu
                130                 135                 140

tat tcc ttg gta cca cta atg tta att gca gga att gtc att tgt gca   541
Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala
            145                 150                 155

ttt tgg gtg tac aga cat cac aag atg gcc tac cct cct gta ctt gtt   589
Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val
        160                 165                 170

cct act caa gac cca gga cca ccc cca cct tcc cca tta cta ggg ttg   637
Pro Thr Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu
    175                 180                 185

aag cca ttg cag ctg tta gaa gtg aaa gca agg gga aga ttt ggt tgt   685
Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys
190                 195                 200                 205

gtc tgg aaa gcc cag ttg ctc aat gaa tat gtg gct gtc aaa ata ttt   733
Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe
            210                 215                 220

cca ata cag gac aaa cag tcc tgg cag aat gaa tat gaa gtc tat agt   781
Pro Ile Gln Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser
            225                 230                 235
```

```
cta cct gga atg aag cat gag aac ata cta cag ttc att ggt gca gag   829
Leu Pro Gly Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu
        240             245             250

aaa aga ggc acc agt gtg gat gtg gac ctg tgg cta atc aca gca ttt   877
Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe
        255             260             265

cat gaa aag ggc tca ctg tca gac ttt ctt aag gct aat gtg gtc tct   925
His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser
270             275             280             285

tgg aat car ctt tgt cat att gca gaa acc atg gct aga gga ttg gca   973
Trp Asn Gln Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala
        290             295             300

tat tta cat gag gat ata cct ggc tta aaa gat ggc cac aag cct gca  1021
Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala
        305             310             315

atc tct cac agg gac atc aaa agt aaa aat gtg ctg ttg aaa aac aat  1069
Ile Ser His Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn
        320             325             330

ctg aca gct tgc att gct gac ttt ggg ttg gcc tta aag ttc gag gct  1117
Leu Thr Ala Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala
        335             340             345

ggc aag tct gca ggt gac acc cat ggg cag gtt ggt acc cgg agg tat  1165
Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr
350             355             360             365

atg gct cca gag gtg ttg gag ggt gct ata aac ttc caa agg gac gca  1213
Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala
        370             375             380

ttt ctg agg ata gat atg tac gcc atg gga tta gtc cta tgg gaa ttg  1261
Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu
        385             390             395

gct tct cgt tgc act gct gca gat gga ccc gta gat gag tac atg tta  1309
Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu
        400             405             410

cca ttt gag gaa gaa att ggc cag cat cca tct ctt gaa gat atg cag  1357
Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln
        415             420             425

gaa gtt gtt gtg cat aaa aaa aag agg cct gtt tta aga gat tat tgg  1405
Glu Val Val Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp
430             435             440             445

cag aaa cat gca gga atg gca atg ctc tgt gaa acg ata gaa gaa tgt  1453
Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys
        450             455             460
```

```
tgg gat cat gat gca gaa gcc agg tta tca gct gga tgt gta ggt gaa   1501
Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu
            465                 470                 475

aga att act cag atg caa aga cta aca aat atc att act aca gag gac   1549
Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp
            480                 485                 490

att gta aca gtg gtc aca atg gtg aca aat gtt gac ttt cct ccc aaa   1597
Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
        495                 500                 505

gaa tct agt cta tgatggtggc accgtctgta cacactgagg actgggactc      1649
Glu Ser Ser Leu
510

tgaactggag ctgctaagct aaggaaagtg cttagttgat tttctgtgtg aaatgagtag  1709

gatgcctcca ggacatgtac gcaagcagcc ccttgtggaa agcatggatc tgggagatgg  1769

atctgggaaa cttactgcat cgtctgcagc acagatatga agaggagtct aagggaaaag  1829

ctgcaaactg taaagaactt ctgaaaatgt actcgaagaa tgtggccctc tccaaatcaa  1889

ggatcttttg gacctggcta atcaagtatt tgcaaaactg acatcagatt tcttaatgtc  1949

tgtcagaaga cactaattcc ttaaatgaac tactgctatt tttttaaat gaaaaacttt   2009

tcatttcaga ttttaaaaag ggtaactttt tattgcattt gctgttgttt ctataaatga  2069

ctattgtaat gccaacatga cacagcttgt gaatgtgtag tgtgctgctg ttctgtgtac  2129

atagtcatca aagtggggta cagtaaagag gcttccaagc attactttaa cctccctcaa  2189

caaggtatac ctcagttcca cggttgttaa attataaaat tgaaaacact aacagaattt  2249

gaataaatca gtccatgttt tataacaagg ttaattacaa attcactgtg ttatttaaga  2309

aaaaatggta agctatgctt agtgccaata gtaagtggct atttgtaaag cagtgtttta  2369

gctttctttc tactggcttg taatttaggg aaaacaagtg ctgtctttga aatggaaaag  2429

aatatggtgt caccctaccc cccatactta tatcaaggtc ccaaaatatt cttttccatt  2489

tcaaagacag cactttgaaa accctaaatt acaagccagt agaagaaaag ctaaaacacg  2549

ctttacaaat agcc                                                   2563
```

<210> 16
<211> 513
<212> PRT
<213> Homo sapiens

<400> 16

```
Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
  1               5                  10                  15
```

Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
       20   25   30

Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
       35   40   45

Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
   50   55   60

Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
65   70   75   80

Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
       85   90   95

Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
       100   105   110

Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
       115   120   125

Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
       130   135   140

Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
145   150   155   160

Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
          165   170   175

Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
        180   185   190

Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
       195   200   205

Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
   210   215   220

Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
225   230   235   240

Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
        245   250   255

Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
        260   265   270

Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Gln
       275   280   285

Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
   290   295   300

Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
305   310   315   320

```
Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
            325             330             335

Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
            340             345             350

Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
            355             360             365

Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
        370             375             380

Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
385             390             395             400

Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
            405             410             415

Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val, Val
            420             425             430

Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
        435             440             445

Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
        450             455             460

Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
465             470             475             480

Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
            485             490             495

Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
            500             505             510

Leu
```